SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Oon, Chong Jin
               Lim, Gek Keow
               Zhao, Yi
               Chen, Wei Ning

   (ii) TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND USES THEREOF

   (iii) NUMBER OF SEQUENCES: 11

   (iv) CORRESPONDENCE ADDRESS:
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   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

   (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: 09/719,528
      (B) FILING DATE: 19-DEC-2000
      (C) CLASSIFICATION: 435

   (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/SG98/00046
      (B) FILING DATE: 19-JAN-1998

   (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Mass, Clifford J.
      (B) REGISTRATION NUMBER: 30,086
      (C) REFERENCE/DOCKET NUMBER: U-014987-0

   (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (212) 708-1800

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 3215 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: circular

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACAACA TTCCACCAAG CTCTGCTAGA TCCCAGGGTG AGGGGCCTAT
ATTTTCCTGC   60

TGGTGGCTCC AGTTCCGGAA CAGTAAACCC TGTTCCGACT ACTGCCTCTC
CCATATCGTC   120

AATCTTCTCG AGGACTGGGG ACCCTGCACC GAACATGGAG AACACAACAT
CAGGATTCCT   180

AGGACCCCTG CTCGTGTTAC AGGCGGGGTT TTTCTCGTTG ACAAGAATCC
TCACAATACC   240

GCAGAGTCTA GACTCTGGTG GACTTCTCTC AATTTTCTAG GGGGAGCACC
CACGTGTTCC   300

TGGCCAAAAT TCGCAGTCCC CAACCTCCAA TCACTCACCA ACCTCTTGTC
CTCCAATTTG   360

TCCTGGCTAT CGCTGGATGT GTCTGCGGCG TTTTATCATA TTCCTCTTCA
TCCTGCTGCT   420

ATGCCTCATC TTCTTGTTGG TTCTTCTGGA CTACCAAGGT ATGTTGCCCG
TTTGTCCTCT   480

ACTTCCAGGA ACATCAACCA CCAGCACGGG GCCATGCAAG ACCTGCACGA
CTCCTGCTCA   540

AGGAAACTCT ACGTTTCCCT CTTGTTGCTG TACAAAACCT TCGGACGGAA
ACTGCACTTG   600

TATTCCCATC CCATCATCCT GGGCTTTCGC AAGATTCCTA TGGGAGTGGG
CCTCAGTCCG   660

TTTCTCCTGG CTCAGTTTAC TAGTGCCATT TGTTCAGTGG TTCGTAGGGC
TTTCCCCCAC   720

TGTTTGGCTT TCAGTTATAT GGATGATGTG GTATTGGGGG CGAAGTCTGT
ACAACATCTT   780

GAGTCCCTTT TTACCTCTAT TACCAATTTT CTTTTGTCTT TGGGTATACA
TTTAAACCCT   840

AATAAAACCA AACGTTGGGG CTACTCCCTT AACTTCATGG GATATGTAAT
TGGAAGTTGG   900

GGTACTTTAC CGCAGGAACA TATTGTACTA AAACTCAAGC AATGTTTTCG
AAAACTGCCT   960

GTAAATAGAC CTATTGATTG GAAAGTATGT CAAAGAATTG TGGGTCTTTT
GGGCTTTGCT   1020

GCCCCTTTTA CACAATGTGG CTATCCTGCC TTGATGCCTT TATATGCATG
TATACAATCT   1080

AAGCAGGCTT TCACTTTCTC GCCAACTTAC AAGGCCTTTC TGTGTAAACA
ATATCTGAAC   1140

CTTTACCCCG TTGCCCGGCA ACGGTCCGGT CTCTGCCAAG TGTTTGCTGA
CGCAACCCCC   1200

ACTGGATGGG GCTTGGCCAT AGGCCATCAG CGCATGGCTG GAACCTTTCT
GGCTCCTCTG   1260

CCGATCCATA CTGCGGAACT CCTAGCAGCT TGTTTGCTC GCAGCCGGTC
TGGAGCAAAA   1320

CTTATCGGAA CCGACAACTC TGTTGTCCTC TCTCGGAAAT ACACCTCCTT
TCCATGGCTG   1380

CTAGGGTGTG CTGCCAACTG GATCCTGCGC GGGACGTCCT TTGTCTACGT
CCCGTCGGCG   1440

CTGAATCCCG CGGACGACCC GTCTCGGGGC CGTTTGGGGC TCTACCGTCC
CCTTCTTCAT   1500

CTGCCGTTCC GGCCGACCAC GGGGCGCACC TCTCTTTACG CGGTCTCCCC
GTATGTGCCT   1560

TCTCATCTGC CGGACCGTGT GCACTTCGCT TCACCTCTGC ACGTCGCATG
GAGACCACCG   1620

TGAACGCACG CCAGGTCTTG CCCAAGGTCT TATATAAGAG GACTCTTGGA
CTCTCAGCAA   1680

TGTCAACGAC CGACCTTGAG GCATACTTCA AAGACTGTGT GTTTAAAGAC
TGGGAGGAGT   1740

TGGGGGAGGA GATTAGGTTA AAGATTTATG TACTAGGAGG CTGTAGGCAT
AAATTGGTCT   1800

GTTCACCAGC ACCATGCAAC TTTTTCTCCT CTGCCTAATC ATCTCATGTT
CATGTCCTAC   1860

TGTTCAAGCC TCCAAGCTGT GCCTTGGGTG GCTTTGGGAC ATGGACATTG
ACCCGTATAA   1920

AGAATTTGGA GCATCTGCTG AGTTACTCTC TTTTTTGCCT TCTGACTTCT
TTCCGTCTAT   1980

TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATCGGGAG GCCTTAGAGT
CTCCGGAACA   2040

TTGTTCGCCT CACCATACAG CACTCAGGCA AGCTATTTTG TGTTGGGGTG
AGTTGATGAA   2100

TCTGGCCACC TGGGTGGGAA GTAATTTGGA AGATCCAGCA TCCAGGGAAT
TAGTAGTCAG   2160

CTATGTCAAC GTTAATATGG GCCTAAAACT CAGACAAATA TTGTGGTTTC
ACATTCCTG   2220

TCTTACTTTT GGAAGAGAAA CTGTTCTTGA GTACTTGGTA TCTTTTGGAG
TGTGGATTCG   2280

CACTCCTACC GCTTACAGAC CACCAAATGC CCCTATCTTA TCAACACTTC
CGGAAACTAC   2340

TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC
GCAGACGAAG   2400

GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAACGTT
AGTATTCCTT   2460

GGACTCATAA GGTGGGAAAC TTTACTGGGC TTTATTCTTC TACTGTACCT
GTCTTTAATC   2520

CCGAGTGGCA AATTCCTTCC TTTCCTCACA TTCATTTACA AGAGGACATT
ATTAATAGAT   2580

GTCAACAATA TGTGGGCCCT CTTACAGTTA ATGAAAAAAG AAGATTAAAA
TTAATTATGC   2640

CTGCTAGGTT TTATCCTAAC CTTACTAAAT ATTTGCCCTT AGACAAAGGC
ATTAAACCGT   2700

ATTATCCTGA ACATGCAGTT AATCATTACT TCAAAACTAG GCATTATTTA
CATACTCTGT   2760

GGAAGGCTGG CATTCTATAT AAGAGAGAAA CTACACGCAG CGCCTCATTT
TGTGGGTCAC   2820

CATATTCTTG GGAACAAGAG CTACAGCATG GGAGGTTGGT CTTCCAAACC
TCGACAAGGC   2880

ATGGGGAGCA ATCTTGCTGT TCCCAATCCT CTGGGATTCT TTCCCGATCA
CCAGTTGGAC   2940

CCTGCGTTCG GAGCCAACTC AAACAATCCA GATTGGGACT TCAACCCCAA
CAAGGATCAC   3000

TGGCCAGAGG CAAATCAGGT AGGAGTGGGA GCATTCGGGC CAGGGTTCAC
CCCACCACAC   3060

GGCGGTCTTT TGGGGGGGAG CCCTCAGGCT CAGGGCATAT TGACAACAGT
GCCAGCAGCA   3120

CCTCCTCCTG CCTCCACCAA TCGGCAGTCA GGAAGACAGC CTACTCCCAT
CTCTCCACCT   3180

CTAAGAGACA GTCATCCTCA GGCCACGCAG TGGAA   3215

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 843 amino acids
        (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1   5   10   15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
           20   25   30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
        35   40   45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
     50   55   60

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Ile Pro Ser Phe Pro
65   70   75   80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
           85   90   95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
           100   105   110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
         115   120   125

Ile Lys Pro Tyr Tyr Pro Glu His Ala Val Asn His Tyr Phe Lys Thr
     130   135   140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145   150   155   160

Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
           165   170   175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
         180   185   190

Gly Asp Glu Ser Cys Cys Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser

195   200   205

Pro Val Gly Pro Cys Val Arg Ser Gln Leu Lys Gln Ser Arg Leu Gly
    210   215   220

Leu Gln Pro Gln Gln Gly Ser Leu Ala Arg Gly Lys Ser Gly Arg Ser
225   230   235   240

Gly Ser Ile Arg Ala Arg Val His Pro Thr Thr Arg Arg Ser Phe Gly
        245   250   255

Gly Glu Pro Ser Gly Ser Gly His Ile Asp Asn Ser Ala Ser Ser Thr
        260   265   270

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Thr Ala Tyr Ser His
    275   280   285

Leu Ser Thr Ser Lys Arg Gln Ser Ser Ser Gly His Ala Val Glu Leu
    290   295   300

His Asn Ile Pro Pro Ser Ser Ala Arg Ser Gln Gly Glu Gly Pro Ile
305   310   315   320

Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp
        325   330   335

Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys
        340   345   350

Thr Glu His Gly Glu His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg
        355   360   365

Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala
    370   375   380

Glu Ser Arg Leu Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
385   390   395   400

Thr Cys Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr
        405   410   415

Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
        420   425   430

Ala Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His Leu Leu

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                435           440           445

Val Gly Ser Ser Gly Leu Pro Arg Tyr Val Ala Arg Leu Ser Ser Thr
    450           455           460

Ser Arg Asn Ile Asn His Gln His Gly Ala Met Gln Asp Leu His Asp
465           470           475           480

Ser Cys Ser Arg Lys Leu Tyr Val Ser Leu Leu Leu Leu Tyr Lys Thr
          485           490           495

Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
          500           505           510

Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
          515           520           525

Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys
    530           535           540

Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val
545           550           555           560

Gln His Leu Glu Ser Leu Phe Thr Ser Ile Thr Asn Phe Leu Leu Ser
          565           570           575

Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser
          580           585           590

Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
    595           600           605

Glu His Ile Val Leu Lys Leu Lys Gln Cys Phe Arg Lys Leu Pro Val
    610           615           620

Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
625           630           635           640

Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
          645           650           655

Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr
          660           665           670
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Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala
        675   680   685

Arg Gln Arg Ser Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr
    690   695   700

Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Ala Gly Thr Phe Leu
705   710   715   720

Ala Pro Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala
    .   725   730   735

Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
        740   745   750

Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
        755   760   765

Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
    770   775   780

Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
785   790   795   800

Leu Leu His Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
        805   810   815

Ala Val Ser Pro Tyr Val Pro Ser His Leu Pro Asp Arg Val His Phe
        820   825   830

Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
    835   840

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 400 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1   5   10   15

Ala Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
            20   25   30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
            35   40   45

Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Val Gly Ala Phe Gly
            50   55   60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Gly Ser Pro Gln
65   70   75   80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
                85   90   95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
                100   105   110

Arg Asp Ser His Pro Gln Ala Thr Gln Trp Asn Ser Thr Thr Phe His
            115   120   125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
            130   135   140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
145   150   155   160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
            165   170   175

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
            180   185   190

Phe Phe Ser Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
            195   200   205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
            210   215   220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro

225   230   235   240

Pro Ile Cys Pro Gly Tyr Arg Trp Asn Cys Leu Arg Arg Phe Ile Ile
        245   250   255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
        260   265   270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
        275   280   285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly
    290   295   300

Asn Ser Thr Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305   310   315   320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
        325   330   335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
        340   345   350

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
        355   360   365

Ile Trp Met Met Trp Tyr Trp Gly Arg Ser Leu Tyr Asn Ile Leu Ser
    370   375   380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
385   390   395   400

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 212 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Leu Phe Leu Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
         20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Ser Ala Glu Leu Leu Ser Phe Leu
         35   40   45

Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser
         50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Asn
             85   90   95

Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala Ser Arg Glu
         100   105   110

Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Leu Arg Gln
         115   120   125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
         130   135   140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Thr Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
             165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
             180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
             195   200   205

Glu Ser Gln Arg
         210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 154 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ala Arg Val Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu
1   5   10   15

Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Val Ser Gly
            20   25   30

Pro Phe Gly Ala Leu Pro Ser Pro Ser Ser Ser Ala Val Pro Ala Asp
        35   40   45

His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser
    50   55   60

Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu
65   70   75   80

Thr Thr Val Asn Ala Arg Gln Val Leu Pro Lys Val Leu Tyr Lys Arg
            85   90   95

Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe
        100   105   110

Lys Asp Cys Val Phe Lys Asp Trp Glu Glu Leu Gly Glu Glu Ile Arg
        115   120   125

Leu Lys Ile Tyr Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser
    130   135   140

Pro Ala Pro Cys Asn Phe Phe Ser Ser Ala
145   150

(2) INFORMATION FOR SEQ ID NO:6:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA   36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA   25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT   25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 32 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT   32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 16 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT   16

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 36 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA   36